

SEQUENCE LISTING

<110> Bayer Aktiengesellschaft

<120> Ligand binding domains of Ultraspiracle (USP) proteins

<130> Le A 34 772

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<150> DE 100 36 461.6

<151> 2000-07-25

<160> 2

<170> PatentIn Ver. 2.1

<210> 1

<211> 262

<212> PRT

<213> Heliothis virescens

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Val Gln Glu Leu Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val  
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Ala Asp Pro Ser Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser  
20 25 30

Asn Val Pro Pro Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile  
35 40 45

Gly Asn Lys Gln Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro  
50 55 60

His Phe Ser Gln Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly  
65 70 75 80

Ser Trp Asn Glu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu  
85 90 95

Phe Leu Thr Glu Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr  
100 105 110

Thr Ser Pro Pro Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His  
115 120 125

Arg Asn Ser Ala Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val  
130 135 140

Leu Ser Glu Leu Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala  
145 150 155 160

Glu Tyr Val Ala Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys  
165 170 175

Gly Leu Lys Asn Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe  
180 185 190

Leu Cys Leu Asp Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly  
195 200 205

Arg Phe Ala Ala Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser  
210 215 220

Leu Lys Ser Phe Glu His Leu Phe Phe His Leu Val Ala Asp Thr  
225 230 235 240

Ser Ile Ala Gly Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro  
245 250 255

Ile Asp Thr Asn Met Met  
260

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<212> PRT  
<213> Heliothis virescens

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Met Ser Val Ala Lys Lys Asp Lys Pro Thr Met Ser Val Thr Ala Leu  
1 5 10 15

Ile Asn Trp Ala Arg Pro Leu Pro Pro Gly Gln Gln Gln Gln Pro Met  
20 25 30

Thr Pro Thr Ser Pro Gly Asn Met Leu Gln Pro Met Ala Thr Pro Ser  
35 40 45

Asn Leu Pro Thr Val Asp Cys Ser Leu Asp Ile Gln Trp Leu Asn Leu  
50 55 60

Glu Gly Gly Phe Met Ser Pro Met Ser Pro Pro Glu Met Lys Pro Asp

65

70

75

80

Thr Ala Met Leu Asp Gly Leu Arg Asp Asp Ser Thr Pro Pro Pro Ala  
 85 90 95

Phe Lys Asn Tyr Pro Pro Asn His Pro Leu Ser Gly Ser Lys His Leu  
 100 105 110

Cys Ser Ile Cys Gly Asp Arg Ala Ser Gly Lys His Tyr Gly Val Tyr  
 115 120 125

Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val Arg Lys Asp  
 130 135 140

Leu Thr Tyr Ala Cys Arg Glu Glu Arg Asn Cys Ile Ile Asp Lys Arg  
 145 150 155 160

Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys Cys Leu Ala Cys  
 165 170 175

Gly Met Lys Arg Glu Ala Val Gln Glu Glu Arg Gln Arg Ala Ala Arg  
 180 185 190

Gly Thr Glu Asp Ala His Pro Ser Ser Ser Val Gln Val Gln Glu Leu  
 195 200 205

Ser Ile Glu Arg Leu Leu Glu Met Glu Ser Leu Val Ala Asp Pro Ser  
 210 215 220

Glu Glu Phe Gln Phe Leu Arg Val Gly Pro Asp Ser Asn Val Pro Pro  
 225 230 235 240

Lys Phe Arg Ala Pro Val Ser Ser Leu Cys Gln Ile Gly Asn Lys Gln  
 245 250 255

Ile Ala Ala Leu Val Val Trp Ala Arg Asp Ile Pro His Phe Ser Gln  
 260 265 270

Leu Glu Met Glu Asp Gln Ile Leu Leu Ile Lys Gly Ser Trp Asn Glu  
 275 280 285

Leu Leu Leu Phe Ala Ile Ala Trp Arg Ser Met Glu Phe Leu Thr Glu  
 290 295 300

Glu Arg Asp Gly Val Asp Gly Thr Gly Asn Arg Thr Thr Ser Pro Pro  
 305 310 315 320

Gln Leu Met Cys Leu Met Pro Gly Met Thr Leu His Arg Asn Ser Ala

325

330

335

Leu Gln Ala Gly Val Gly Gln Ile Phe Asp Arg Val Leu Ser Glu Leu  
340 345 350

Ser Leu Lys Met Arg Thr Leu Arg Val Asp Gln Ala Glu Tyr Val Ala  
355 360 365

Leu Lys Ala Ile Ile Leu Leu Asn Pro Asp Val Lys Gly Leu Lys Asn  
370 375 380

Arg Gln Glu Val Glu Val Leu Arg Glu Lys Met Phe Leu Cys Leu Asp  
385 390 395 400

Glu Tyr Cys Arg Arg Ser Arg Ser Ser Glu Glu Gly Arg Phe Ala Ala  
405 410 415

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Ser Leu Lys Ser Phe  
420 425 430

Glu His Leu Phe Phe His Leu Val Ala Asp Thr Ser Ile Ala Gly  
435 440 445

Tyr Ile Arg Asp Ala Leu Arg Asn His Ala Pro Pro Ile Asp Thr Asn  
450 455 460

Met Met  
465